a1 A57410 (Ho, S.N. et. al., 1995, J. Biol. Chem. 270 (34), 19898-19907), AAA93249 (U28807), NP_004546 (NM_004555)].

Concluded

a2 Fig. 11 shows the alignment of amino acid sequences (SEQ ID NOS 8-11, respectively, in order of appearance) in N-terminal domains of human members of the NFAT polypeptide family. Sequences for NFAT1 (Luo, C.E. et al., 1996, Mol. Cell. Biol. 16: 3955-66), NFATc (Northrop, J.P. et al., 1994, Nature 369:497-502), NFATx (Hoey, T. et al., 1995, Immunity 2: 461-72; Masuda, E.S. et al., 1995, Mol. Cell. Biol. 15: 2697-706), and NFAT3 (Hoey, T. et al., 1995, Immunity 2:461-72) were aligned by using the Lasergene Megalign program (DNAstar, Madison, Wis.), with additional adjustments. Residues are numbered on the right and end at sequences corresponding to the start of their RSDs. Consensus residues, shown above the alignment, are a 100% match for the residue group. Residue groupings were as follows: DE; HKR; AGILV; NQ; FWY; ST; P; CM. Residues that match the consensus are shaded (with solid black).

Respectfully submitted,

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MARKED-UP VERSION OF THE SPECIFICATION

Fig. 10 shows the alignment of amino acid sequences in N-terminal domains of NF-ATx polypeptide family. mNFATx; mouse NFATx (SEQ ID NO: 5) [Ac. No. BAA12833 (D85612)], hNFATx (SEQ ID NO: 6); human NFATx [Ac. No. AAC27434 (AC004531), AAB46597 (U85430), AAB46596 (U85429), AAB46595 (U85428), AAA86308 (U14150)], NFATc3 (SEQ ID NO. 7); human and mouse NFATc3 [pir: locus A57410 (Ho, S.N. et. al., 1995, J. Biol. Chem. 270 (34), 19898-19907), AAA93249 (U28807), NP_004546 (NM_004555)].

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